Role of poplar DNA demethylases in controlling winter dormancy

Daniel Conde, Alicia Moreno-Cortés, Tamara Hernández-Verdeja, Jose M. Ramos-Sánchez, Mariano Perales, Pablo González-Melendi and Isabel Allona.

Centro de Biotecnología y Genómica de Plantas (CBGP, UPM-INIA). Departamento de Biotecnología-Biología Vegetal. Universidad Politécnica de Madrid. Campus de Montegancedo, 28223-Pozuelo de Alarcón (Madrid), España

daniel.conde@upm.es

Trees have developed the mechanism of winter dormancy to survive the harsh conditions of winter in temperate and cold regions. It determines the geographical distribution of tree species and the long of the growing period. Epigenetic control of winter dormancy in woody plants is barely known. 5-methyl cytosine (5mC) is an important epigenetic mark that regulates gene expression in animals and plants. The profile of DNA methylation changes in the transition of developmental stages in plants such as chestnut bud set and burst, flowering in azalea, aging in pine trees among other. So far, the enzymes involved in the modification of the methylome and the molecular mechanism behind the control over those development processes remain to be understood. Our previous results showed higher DNA methylation and less acetylated Lys 8 of histone H4 global levels in poplar stem during winter dormancy compared to active growing season. Analysis of the 5-methyl cytosine levels by the application of the immunofluorescence-based method set up in our lab showed that global DNA methylation decrease significantly when trees are near to restore the growing season after the winter dormancy. We have identified two poplar homologs to Arabidopsis *DME* gene: *PtaDML8/PtaDML10*. DME protein promotes global DNA demethylation along the genome during the endosperm development. Our RT-PCR analyses indicate that the expression of *PtaDML8/PtaDML10* genes increases significantly when trees are near to restart growing after the winter. Functional characterization showed that PtaDML8/PtaDML10 knockdown plants have a delayed in resuming of growth after dormancy.
Taken together, we hypothesize that an active control of the 5mC DNA methylation play a key role in winter dormancy and that 5mC demethylases would be crucial for poplar dormant-growth transition.

Acknowledgements

This work was funded by the Spanish Ministry of Science and Innovation AGL2011-22625/FOR and by KBBE "Tree for Joules" PIM2010PKB-00702. Fellowships: A.M-C. was partly supported by the JC postdoctoral program from the Universidad Politécnica de Madrid (JC/03/2010). JL.G-P. was supported by a Marie-Curie Cofund Fellowship. M.P. is supported by the Ramon y Cajal program of Ministerio de Economía y Competitividad (RYC-2012-10194).